In the Specification:

Please amend the specification as shown:

Please delete the paragraphs on page 6, lines 5-10 and replace them with the following amended paragraphs:

FIGS. lA and 1B are hairpin decoys. Hairpin decoys are single oligonucleotides containing self-complementary sequences that self-hybridize to form a partial duplex with a 5' extension or tail and a 3' end that cannot be extended by polymerase. **The left column of Figure 1A discloses SEQ ID NOS 11, 11, 12, 12, 13, 13, 14, 14, 10 and 10, respectively, in order of appearance. The right column of Figure 1A discloses SEQ ID NOS 15, 15, 16, 16, 17, 17, 18 and 18, respectively, in order of appearance. The left column of Figure 1B discloses SEQ ID NOS 19-25, 19, 19, 20, 20, 21, 21, 22, 22, 23, 23, 24, 24, 25 and 25, respectively, in order of appearance. The right column of Figure 1B discloses SEQ ID NOS 12 and 12.**

FIG. 2 illustrates duplex decoys. Duplex decoys are formed by hybridizing two oligonucleotides containing complementary sequences to form a partial duplex with a 5' extension or tail and a 3' end that cannot be extended by polymerase. **Figure 2 discloses SEQ ID NOS 26, 4, 27-28, 7, 6, 5 and 29-37, respectively, in order of appearance.**

Please delete the paragraphs on page 19, line 20 to page 20, line 16 and replace them with the following paragraphs:

Demonstration of decoy effects on primer-dimer formation in real time PCR. Reactions were set-up as follows: 1 ul 10x PCR buffer (100 mM BTP pH9.1, 400 mM KAc, 20 mM MgC12, 1 mg/ml BSA), 100 uM each dATP, dTTP, dCTP, dGTP (Promega), 3 uM dabcyl iGTP (EraGen Biosciences), 200 nM forward PCR primer CL025 (5' FAM-TXGATAGCAACAATTCATCTACAGA) **(SEQ ID NO: 1)**, 200 nM reverse PCR primer CL026 (5' ATGGGTAGTGAATGATCTTGTTTC) **(SEQ ID NO: 2)**, 1 U KlenTaq (Ab peptides) and 5 ul synthetic DNA target CL021 (5' TCAGATAGCAACAATTCATCTACAGA-CCCAATTAGCAGTGGAGAAACAAGATCATTCACTACCCATTTCTTAACTTATCCCAA GATAGGACTTCTGTACA) **(SEQ ID NO: 3)**. A dilution series consisting of concentrations ranging from 100,000 to 0.1 molecules, plus a no target control was amplified in the presence of

no decoy (Fig 5A), 5 uM MM309/310 (Fig 5B), 5 uM MM309/311(Fig 5C),, and 5 uM MM309/312 (Fig 5D). The PCR thermocycling was performed in an iCycler (Bio-Rad) with the following cycling conditions: 2 minute 94° denature, PCR 60 rounds: 1 sec 94°; 1 sec 58°; 20 sec 72° with optical reading. After PCR cycling a melt analysis was performed. The samples were heated from 60° to 95° with optical reads at every 0.5° increment.

5′ GCTGTCTGGTCCGTTATTATAC - PO4 **(SEQ ID NO: 4)** MM309

3′ **ddC[[C]]**AATAATATG **(SEQ ID NO: 5)** MM310 Tm = 24.3°

3′ **ddC**AGGCAATAATATG **(SEQ ID NO: 6)** MM311 Tm = 40.5°

3′ **ddC**CAGGCAATAATATG **(SEQ ID NO: 7)** MM312 Tm = 45°

Example 2

Selective inhibition of MMLV reverse transcriptase.

CL001

GCTGTCTGGTCCGAAACGATCGGGATTTTTTTTTAAAATCCCGATCGTTTCdd **(SEQ ID NO: 8)**

CL002

GCTGTCTGGTCCGAAACGATCGGGATTTTTTTTTAAAATCCCGATCGTTTCdd **(SEQ ID NO: 9)**

(UNDERLINED BASES ARE 2'O-methyl)

DM436 FAM-TXAGAGTCTGGTGCCGACTCGACGTTTTCGTCGAGTCG **(SEQ ID NO: 10)**